

SEQUENCE LISTING

1. GENERAL INFORMATION:

i. APPLICANT: Alimcher, Laurie H. et al.

ii. TITLE OF INVENTION: Human c-Maf Compositions and
Methods of Use Thereof

iii. NUMBER OF SEQUENCES: 2

iv. CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD, LLP
(B) STREET: 28 State Street
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109

v. COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

vi. CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

vii. PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/030,579
(B) FILING DATE: 2-FEB-1998

viii. ATTORNEY/AGENT INFORMATION:

(A) NAME: Kara, Catherine J.
(B) REGISTRATION NUMBER: 41,106
(C) REFERENCE/DOCKET NUMBER: HUI-027CP

ix. TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617)227-7400
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

A NAME KEY: YTD
B LOCATION: 1111233

5 81 SPIDERHOLE PROPHETIC: SEQ ID N 111

ATG GAA TTA GAA CTG GAA ATG AAT AAT TCG GAG CTG GAA AAT AAT AAT
48
Met Ala Ser Ile Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro
10 1 5 10 15

TTG GGC ATG GAA TAT GTT AAT GAG TTC CAT CTG ATG AAG TTT GAA TCG
76
Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
15 20 25 30

AAA AAG GAA CCG GTG GAG AAG GAG GGC ATC ATC AAG CAG TCG GAT CAT
144
Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
20 35 40 45

CTC ATC GCC GGG GGC TCG CTG TCC TCC ACC CCC ATG AGC ACG CCC TAT
192
Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
25 50 55 60

AGC TCG GTG CCC CCG TCC CCC AGC TTC TCG GCG CCC AGC CCG GGC TCG
240
Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
30 65 70 75 80

CGA GGC GAA CAG AAG GCG CAC CTG GAA GAC TAC TAC TGG ATG ACC GGC
288
Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
35 85 90 95

TAC CCG CAG CAG CTG AAC CCC GAG GCG CTG GGC TTC AGC CCC GAG GAC
336
Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
40 100 105 110

GCG GTC GAG GCG CTC ATC AGC AAC AGC CAC CAG CTC CGG GGC GGC TTC
384
Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe
45 115 120 125

GAT GGC TAT GCG CGC GGG GCG CAG CAG CTA GCC GCG GCG GCC GGG GCA
432
Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Ala Gly Ala
50 130 135 140

GGT GCC GGC GCC TCC TTG GGC GGC AGC GGC GAG GAG ATG GGC CCC GCC
480
Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala
55 145 150 155 160

123 GGC TTA TTS TCG GAG GTG ATA GAC AAA AGG GCG TTA CAG AAT GGC
 124
 Ala Ala Val Val Leu Ala Val Ile Ala Ala Ala Ala Ala His Ser Gly
 125 126 127
 5 TTA GGT TTA TAC TAC CAC CAC CAC CAC CAC CAC GGT TTA TGC CAC CAC
 128
 Ala Gly Ile His Tyr His His His His His His Ala Ala Gly His His
 129 130 131
 10 CAC CAC CCG ACG GCC GGC GCG CCC GGC GCC GTG GGC AGC GCG GCC GGT
 132
 His His Ile Thr Ala Gly Ala Ile Gly Ala Ala Gly Ser Ala Ala Ala
 133 134 135
 15 TCG GCC GGT GGC GGT GGG GGC GCG GGC GGC GGT GGC CCG GCC AGC GTT
 136
 Ser Ala Gly Gly Ala Gly Gly Ala Gly Gly Gly Gly Ile Ala Ser Val
 137 138 139
 20 GGG GGC GGC GGC GGC GGC GGC GGC GGC GGA GGC GGC GGC GGC GGC
 140
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala
 141 142 143
 25 GGC GCC CTG CAC CCG CAC CAC GCC GCC GGC GGC CTG CAC TTC GAC GAC
 144
 Gly Ala Leu His Pro His His Ala Ala Gly Gly Leu His Phe Asp Asp
 145 146 147
 30 CGC TTC TCC GAC GAG CAG CTG GTG ACC ATG TCT GTG CCG GAC TGG AAC
 148
 Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Asp Trp Asn
 149 150 151
 35 CGG CAG CTG CGC GGG GTC AGC AAG GAG GAG GTG ATC CGG CTG AAG CAG
 152
 Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln
 153 154 155
 40 AAG AGG CGG ACC CTG AAA AAC CGC GGC TAT GCC AAG TCC TGC CGC TTC
 156
 Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe
 157 158 159
 45 AAG AGG GTG CAG CAG AGA CAC GTC CTG GAG TCG GAG AAG AAC CAG CTG
 160
 Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu
 161 162 163
 50 CTG CAG CAA GTC GAC CAC CTC AAG CAG GAG ATC TCC AGG CTG GTG CGC
 164
 Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg
 165 166 167
 55 GAG AGG GAC GCG TAC AAG GAG AAA TAC GAG AAG TTG GTG AGC AGC GGC
 168
 1056

His Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly
 340 345 350
 5 TTC CCA GAA AAC GGC TCG AGC AGC GAC AAC CCG TAC TCT CCC GAG TTT
 1104
 Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe
 355 360 365
 10 TTC ATA ACT GAG CCC ACT CGC AAG TTG GAG CCA TCA GTG GGA TAC GCC
 1152
 Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala
 370 375 380
 15 ACA TTT TGG AAG CCC CAG CAT CGT GTA CTT ACC AGT GTG TTC ACA AAA
 1200
 Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys
 385 390 395 400
 20 TGA
 1203

25 (C) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 amino acids
 (B) TYPE: amino acid
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ser Glu Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro
 1 5 10 15
 40 Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
 20 25 30
 Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
 35 40 45
 45 Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
 50 55 60
 Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
 65 70 75 80
 5 Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
 85 90 95
 55 Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
 100 105 110
 Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe

	115	120	125
	Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Ala Gly Ala		
	130	135	140
5	Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala		
	145	150	155 160
	Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Ala Gln Ser Gly		
10		165	170 175
	Ala Gly Pro His Tyr His His His His His His Ala Ala Gly His His		
	180	185	190
15	His His Pro Thr Ala Gly Ala Pro Gly Ala Ala Gly Ser Ala Ala Ala		
	195	200	205
	Ser Ala Gly Gly Ala Gly Gly Ala Gly Gly Gly Gly Pro Ala Ser Val		
20	210	215	220
	Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala		
	225	230	235 240
	Gly Ala Leu His Pro His His Ala Ala Gly Gly Leu His Phe Asp Asp		
25		245	250 255
	Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Asp Trp Asn		
	260	265	270
30	Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln		
	275	280	285
	Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe		
35	290	295	300
	Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu		
	305	310	315 320
	Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg		
40		325	330 335
	Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly		
	340	345	350
45	Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe		
	355	360	365
	Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala		
50	370	375	380
	Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys		
	385	390	395 400